

DKGR-SEQS.ST25.txt

<210> 3  
<211> 843  
<212> DNA  
<213> *Corynebacterium* species

<220>  
<221> misc\_feature  
<223> "n" positions at both ends of sequence represent restriction endo nuclease recognition sites; "n" positions at residues 49-51, and 55-57 represent areas of disagreement in the published sequence for wild type DKGR-B between Sonoyama and Powers, however, both published sequences encode the same amino acid

<400> 3  
nnnatgccga acatccccac catcagcctc aacgacggac gccccttcnn ngagnnnnggg 60  
ctcggcacgt acaacctgcg cggcgcacgag ggggtcgccg ccatggtcgc cgcgatcgac 120  
tcgggctacc gcctgctcga cacggcggtg aactacgaga acgagagcga ggtcgccga 180  
gcgggtgcgcg cgagcagcgt cgatcgcac gagctcatcg tggcgagcaa gatcccggc 240  
cgccagcacg ggcgcgcccga ggcggtcgac agcatccgcg gatcgctcga ccggctgggg 300  
ctcgacgtga tcgacactgca gctgatccac tggccgaacc ccagcgtggg ccggtggtc 360  
gacacctggc gcgccatgtat cgacgcgcgc gaggcgggcc tggtccgcctc gatcgccgtc 420  
tcgaacttca ccgagccgtat gctgaagacc ctcatcgacg agaccgggtt cacaccgcg 480  
gtcaaccagg tcgagactcca cccgtacttc ccccaggcgg cgctgcgcgc gttccacgac 540  
gagcacggca tccgcaccga gagctggagc ccgctcgccc ggcgcagcga gctgctcacc 600  
gagcagctgc tgcaggagct ggcggtcgtc tacggagtga cgccgacgca ggtggtgctg 660  
cggtggcacg tgcagactcgg cagcaccccg atccccaaat ccgcccaccc cgatcgccag 720  
cgcgagaacg ccgatgtgtt cggcttcgcc ctcaccgcgc accaggtcga tgcgatctcg 780  
ggcctcgagc gcggggcggtctt ctgggacggc gacccgcaca cgacgaaaga gatgtagnnn 840  
nnnn 843

<210> 4  
<211> 843  
<212> DNA  
<213> *Corynebacterium* species

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<400> 4  
catatgccga acatcccgac catctctctg aacgacggtc gtccgttccc ggaactgggt 60  
ctgggtacct acaacacctgcg tggtgacgaa ggtgttgctg ctatggttgc tgctatcgac 120  
tctggttacc gtctgctgga caccgctgtt aactacgaaa acgaatctga agttggtcgt 180  
gctgttcgtg cttcttctgt tgaccgtgac gaactgatcg ttgcttctaa aatccgggt 240  
cgtcagcacg gtcgtgctga agctgttgc tctatccgtg gttctctgga ccgtctgggt 300  
ctggacgtta tcgacactgca gctgatccac tggccgaacc cgctgttgg tcggtggctg 360  
gacacctggc gtggtatgat cgacgctcgta gaagctggtc tgggtcggtc tatcggtgtc 420  
tctaacttca ccgaaccgat gctgaaaacc ctgatcgacg aaaccgggtgt tacccggct 480  
gttaaccagg ttgaactgca cccgtacttc ccgcaggctg ctctgcgtgc tttccacgac 540  
gaacacggta tccgtaccga atcttggtct ccgcaggctc gtcgttctga actgctgacc 600  
gaacagctgc tgcaggaact ggctgttgtt tacgggttta ccccgaccca ggttggctg 660  
cggtggcacg ttcagctggg ttctaccccg atccgaaat ctgctgaccc ggaccgtcag 720  
cgtgaaaacg cagacgtttt cggttcgct ctgaccgctg accaggttga cgctatctct 780  
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ctt 843

<210> 5

<211> 277

<212> PRT

<213> *Corynebacterium* species

<400> 5

Met	Thr	Val	Pro	Ser	Ile	Val	Leu	Asn	Asp	Gly	Asn	Ser	Ile	Pro	Gln
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Leu	Gly	Tyr	Gly	Val	Phe	Lys	Val	Pro	Pro	Ala	Asp	Thr	Gln	Arg	Ala
								25					30		
Val	Glu	Glu	Ala	Leu	Glu	Val	Gly	Tyr	Arg	His	Ile	Asp	Thr	Ala	Ala
							35	40			45				
Ile	Tyr	Gly	Asn	Glu	Glu	Gly	Val	Gly	Ala	Ala	Ile	Ala	Ala	Ser	Gly
							50	55			60				
Ile	Ala	Arg	Asp	Asp	Leu	Phe	Ile	Thr	Thr	Lys	Leu	Trp	Asn	Asp	Arg
							65	70		75			80		
His	Asp	Gly	Asp	Glu	Pro	Ala	Ala	Ile	Ala	Glu	Ser	Leu	Ala	Lys	
							85		90			95			

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Leu Ala Leu Asp Gln Val Asp Leu Tyr Leu Val His Trp Pro Thr Pro  
100 105 110  
Ala Ala Asp Asn Tyr Val His Ala Trp Glu Lys Met Ile Glu Leu Arg  
115 120 125  
Ala Ala Gly Leu Thr Arg Ser Ile Gly Val Ser Asn His Leu Val Pro  
130 135 140  
His Leu Glu Arg Ile Val Ala Ala Thr Gly Val Val Pro Ala Val Asn  
145 150 155 160  
Gln Glu Leu His Pro Ala Tyr Gln Gln Arg Glu Ile Thr Asp Trp Ala  
165 170 175  
Ala Ala His Asp Val Lys Ile Glu Ser Trp Gly Pro Leu Gly Gln Gly  
180 185 190  
Lys Tyr Asp Leu Phe Gly Ala Glu Pro Val Thr Ala Ala Ala Ala  
195 200 205  
His Gly Lys Thr Pro Ala Gln Ala Val Leu Arg Trp His Leu Gln Lys  
210 215 220  
Gly Phe Val Val Phe Pro Lys Ser Val Arg Arg Glu Arg Leu Glu Glu  
225 230 235 240  
Asn Leu Asp Val Phe Asp Phe Asp Leu Thr Asp Thr Glu Ile Ala Ala  
245 250 255  
Ile Asp Ala Met Asp Pro Gly Asp Gly Ser Gly Arg Val Ser Ala His  
260 265 270  
Pro Asp Glu Val Asp  
275

<210> 6

<211> 277

<212> PRT

<213> *Corynebacterium* species

<400> 6

Met Pro Asn Ile Pro Thr Ile Ser Leu Asn Asp Gly Arg Pro Phe Pro  
1 5 10 15  
Glu Leu Cys Leu Gly Thr Tyr Asn Leu Arg Gly Asp Glu Gly Val Ala  
20 25 30  
Ala Met Val Ala Ala Ile Asp Ser Gly Tyr Arg Leu Leu Asp Thr Ala  
35 40 45  
Val Asn Tyr Glu Asn Glu Ser Glu Val Gly Arg Ala Val Arg Ala Ser  
50 55 60  
Ser Val Asp Arg Asp Glu Leu Ile Val Ala Ser Lys Ile Pro Gly Arg  
65 70 75 80

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Gln His Gly Arg Ala Glu Ala Val Asp Ser Ile Arg Gly Ser Leu Asp  
85 90 95  
Arg Leu Gly Leu Asp Val Ile Asp Leu Gln Leu Ile His Trp Pro Asn  
100 105 110  
Pro Ser Val Gly Arg Trp Leu Asp Thr Trp Arg Gly Met Ile Asp Ala  
115 120 125  
Arg Glu Ala Gly Leu Val Arg Ser Ile Gly Val Ser Asn Phe Thr Glu  
130 135 140  
Pro Met Leu Lys Thr Leu Ile Asp Glu Thr Gly Val Thr Pro Ala Val  
145 150 155 160  
Asn Gln Val Glu Leu His Pro Tyr Phe Pro Gln Ala Ala Leu Arg Ala  
165 170 175  
Phe His Asp Glu His Gly Ile Arg Thr Glu Ser Trp Ser Pro Leu Ala  
180 185 190  
Arg Arg Ser Glu Leu Leu Thr Glu Gln Leu Leu Gln Glu Leu Ala Val  
195 200 205  
Val Tyr Gly Val Thr Pro Thr Gln Val Val Leu Arg Trp His Val Gln  
210 215 220  
Leu Gly Ser Thr Pro Ile Pro Lys Ser Ala Asp Pro Asp Arg Gln Arg  
225 230 235 240  
Glu Asn Ala Asp Val Phe Gly Phe Ala Leu Thr Ala Asp Gln Val Asp  
245 250 255  
Ala Ile Ser Gly Leu Glu Arg Gly Arg Leu Trp Asp Gly Asp Pro Asp  
260 265 270  
Thr His Glu Glu Met  
275